

09/720841

## The erythromycin PKS

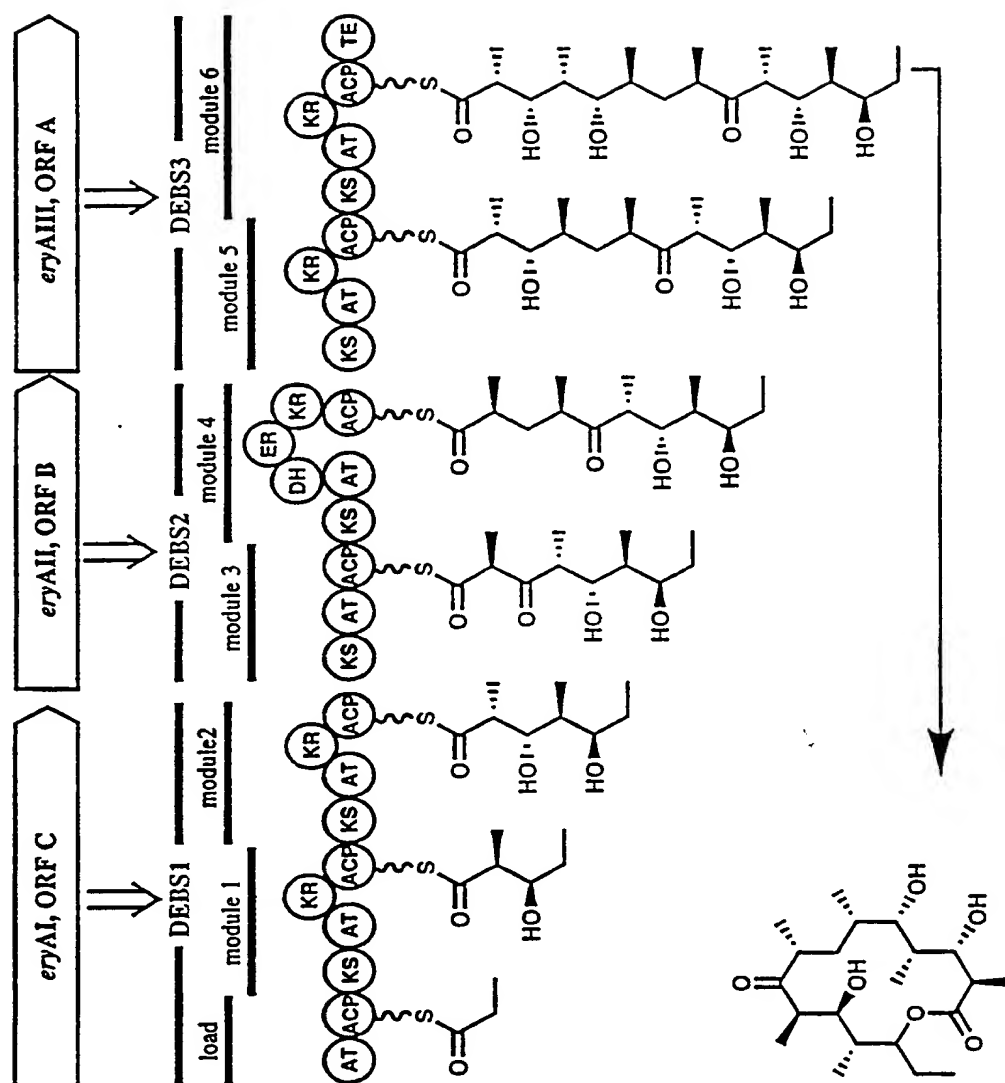


Fig. 1

09/720841

KCLFDAU  
KCLFPEU  
KCLFACT  
KCLFHIR  
KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE  
KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

-----MVTGLGIVAPNGLGVGAIWDAVLNNGRNGIGPLR  
MTGTAARTASSQLHASPAGRRGLRGRAVVTGLGIVAPNGLGVGAYWDAVLNNGRNGIGPLR  
-----MSVLITGVGVVAPNGLGLAPYWSAVLDGRHGLGPVT  
-----MSTWVTGMGVVAPNGLGADDHWAATLKGRHGISRLS  
-----MSTPDRRRRAVVTGLSVAAPGGLGTERYWKSLLTGENGLAELS  
-----MTAAVVVTGLGVVAPTGLGVREHWSSTVRGASAIGPVT  
-----MSAPAPVVVTGLGIVAPNGTGTEEYWAATLAGKSGIDVIO  
-----MTP-VAVTGMGLAAPNGLGRPTTGRPPWAPRAASAAT  
-----MSASVVVTGLGVAAPNGLGREDFWASTLGKSGIGPLT  
-----MSGPQRTGTGGSSRAVVTGLGVLSPHGTGVEAHKAVADGTSLSGPVT  
-----MTRRVVITGVGVRAVPGGSGTKEFWDLLTAGRTATRPIS  
-----MTRRVVITGVGVRAVPGGLGAKNFWELLTSGRTATRRIS  
-----MKRRVVITGVGVRAVPGGNGTRQFWELLTSGRTATRRIS  
-----MTQRRVAITGIEVLAPGGLGRKEFWQLLSEGRATATRGIT  
-----MTARRVVITGIEVLAPGGTGSKAFWNLLSEGRATATRGIT  
-----MKESINRRVVITGIGIVAPDATGVKPFWDLLTAGRTATRTIT  
-----MTRHAEKRVVITGIGVRAVPGGAGTAAFWDLLTAGRTATRTIS  
-----MNRVVITGMGVVAPGAIGIKSFWELLLSGTTATRAIT  
-----MNRIVITGIGVVAPGAVGTPKFWELLLSGTTATRAIS  
-----MTRRRVAVTGIGVVAPGGIGTPQFWELLSEGRATATRRIS

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KCLFDAU  
KCLFPEU  
KCLFACT  
KCLFHIR  
KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE  
KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

RFADDGRLGRLAGEVSDFVP-EDHLPKRLLVQTDPMQMTALAAAEWALREAGCAPSS--  
RFTGDGRLGRLAGEVSDFVP-EDHLPKRLLAQTDPMQY-ALAAAEWALRESGCSPSS--  
RFDVSRYPATLAGQIDDFHA-PDHPGRLLPQTDPPSTR-ALTAADWALQDAKADPES-L  
RFDPTGYPAELAGQVLDFDA-TEHLPKRLLPQTDVSTRF-ALAAAWALADAEDVPAE-L  
RFDASRYPSRLAGQIDDFEA-SEHLP SRLLPQTDVSTRY-ALAAADWALADAGVGPESGL  
RFDAGRYPSKLAGVPGFVP-EDHLP SRLMPQTDHMTL-ALVAADWAFQDAVDP SK-L  
RFDPHGYPV RVGGEVLAFDA-AAHLPGRLLPQTDRTQH-ALVAAEWALADAGLEPEK-Q  
RFDPSGYPAQLAGEIPGFRA-AEHLPGRLVPQTDRTVTRL-SLAAADWALADAGVEVAA-F  
RFDPTGYPARLAGEVPGFAA-EEHLP SRLLPQTDRTMTRL-ALVAADWALADAGVRPEE-Q  
REGCAHLPLRVAGEVHGFDA-AETVEDRFLVQTDRTFTHF-ALSATQH ALADARFGRADVD  
FFDASPFRSRIAGEI-DFDAVAEGFSPREVRMDRATQF-AVACTRDALADSGLDGTGA-L  
FFDPTPNRSQIAAEC-DFDPEHEGLSPREIRMDRAAQF-AVVCTRDAVADSGLEFEQ-V  
FFDPSPYRSQVAAEA-DFDPVAEGFGPRELDRMDRASQF-AVACAREFAASGLDPDT-L  
FFDPAPFRSKVAAEA-DFCGLENGSLPQEVRRMDRAAQF-AVV TAR-AVEDSGAELAA-H  
FFDPTPFRSRVAAEI-DFDPEAHGLSPQEIIRMDRAAQF-AVVAAR-AVADSGIDLAA-H  
AFDPSPF RSRIAAEC-DFDPLAEGLTPOQIRMDRATQF-AVVSARESLED SGDLGA-L  
LFDAAPYRSRIAGEI-DFDPIGEGLSRQASTYDRATQL-AVVCAREALKDSGLDPAA-V  
TFDATPFRSRIAAEC-DFDPVAAGLSAEQARRLDRAQF-ALVAGQEALTD SGLRIGE-D  
TFDATPFRSRIAAEC-DFDPVAAGLSAEQARRLDRAQF-ALVAGQEALADSGLRIDE-D  
LFDPSGLRSQIAAEC-DFEPSDHGLGLATAQRCDRYVQF-ALVAASEAVRDANLDMNR-E

: \* : : \* : : : \*

Fig 2A

09/720841

KCLFDAU  
KCLFPEU  
KCLFACT  
KCLFHIR  
KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE  
KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

-PLEAGVITASASGGFASGQRELQNLWSKG-----PAHVSAYMSFAWFY-AVNTGQIAIR  
-PLEAGVITASASGGFAFGQRELQNLWSKG-----PAHVSAYMSFAWFY-AVNTGQIAIR  
TDYDMGVVTANACGGFDFTHREFRKLWSEG-----PKSVSVYESFAWFY-AVNTGQISIR  
PEYGTGVITSNATGGFEFTHREFRKLWAQG-----PEFVSVYESFAWFY-AVNTGQISIR  
DDYDLGVVTSTAQGGFDFTHREFHKLWSQG-----PAYVSVYESFAWFY-AVNTGQISIR  
PEYGVGVVTASSAGGFEEFGHRELQNLWSLG-----PQYVSAYQSFADFY-AVNTGQVSIR  
DEYGLGVLTAAAGAGGFEEFGQREMOKLWGTG-----PERVSAYQSFADFY-AVNTGQISIR  
DPLDMGVVTASHAGGFEEFGQDELOKLLGQG-----QPVL SAYQSFADFY-AVNSGQISIR  
DDFDMGVVTASASGGFEFGQELQKLWSQG-----SQYVSAYQSFADFY-AVNSGQISIR  
SPYSVGVTAAAGSGGGFEFGQRELQNLWGHG-----SRHVGYPYQSIADFY-AASTGQVSIR  
DPSRIGVALGSASASATSLENEYLVMSDSGREWLVDPAHLSPTMFDYLSPGVMPAEVAWA  
PPERIGVSLGSASAAATSLAQEYLVLSDGGREWQVDPAYLSAHMFDYLSPGVMPAEVAWT  
DPAVGVSLGSASAAATSLEREYLLLSDSGRDWEVDAAWLSRHMFYDLPVSPVMPAEVAWA  
PPHRIGVVVGSAVGATMGLDNEYRVVSDGGRLDLVDHRYAVPHLYNYLVPSSFAAEVAWA  
DPYRVGVTVGSAGVATMGLDEEYRVVSDGGRLDLVDHAYAVPHLYDMYVPSFSAEVAWA  
DASRTGVTVGSAGVATMGLDEEYRVVSDGGRLDLVDHAYAVPHLYDMYVPSFSAEVAWA  
NPERIGVSI GTAVGCTTGLDREYARVSEGGSRWLVDHITLAVEQLFDYFVPTSICREVAWE  
SAHRVGVCVGTAVGCTQKLESEYVALSAGGANWVDPHGRAPELYDYFVPSLAAEVAWL  
SAHRVGVCVGTAVGCTQKLESEYVALSAGGAHWVDPGRGSPELYDYFVPSLAAEVAWL  
DPWRAGATLGTAVGGTTRLEHDYVLVSEGRSRWDVDDRSEPHLERAFTPATLSASAAEE



KCLFDAU  
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KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE  
KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

-HDLRGPVGVVVAEQAGGLDALAHAR-RKVRGGAE-LIVSGAMDSLCP-YGMAAQVRSG  
-HDLRGPVGVVVAEQAGGLDALAHAR-RKVRGGAE-LIVSGAVDSLCP-YGMAAQVKS  
-HGMRGPSALVAEQAGGLDALGHAR-RTIRRGTP-LVVSAGVDSALDP-WGWSVQIASG  
-HGLRGPVSVLVAEQAGGLDAVGHGG--AVRNGTP-MVVTGGVDSFDP-WGWSVSHVSSG  
-NIMRGPSAALVGEQAGGLDAIGHAR-RTVRRGPG-WCSAVASTRRSTR-GASSSQLSGG  
-HGLRGPVGVLTVEQAGGLDALGOAR-RQLRRGLP-MVAVAGVDGSPCP-WGWSVQIASG  
-HGMRGHSSVFTVEQAGGLDAAAHAA-RLLRKGTLTALTGGCEASLCP-WGLVAQIPSG  
-HGMKGPSGVVVSQAGGLDALAQAR-RLVRKGTP-LIVCGAVEPRSPAGAGSPSSPAGG  
-NGMKGPSGVVVSQAGGLDAVAQAR-RQIRKGT-TRIVSGGVDSALCP-WGWSVQIASG  
-NDFKGPVGVVVAEAGGLDALAHAA-LAVRNGTD-TVVCGATEAPLAP-YSTVCQLGYP  
-AGAEGPVTMVSDGCTSGLDVSGYAV-QGTREGSADVVVAGAADTFVSPITVACFDAIKA  
-VGAEGPVAMVSDGCTSGLDLSLHAC-SLIAEGTTDMVAGAADTFITPITVACFDAIKA  
-VGAEGPVTMVSTGCTSGLDVSGNAV-RAIEEGSADVMFAGAADTFITPITVACFDAIRA  
-VGAEGPSTVSTGCTSGLDVAGIAY-ELVREGSADVMVAGAVDAPISPIP-CVLDAIKA  
-VGAEGPNTVSTGCTSGLDVSGYARGELIREGSADVMLAGSSDAPISPIITMACFDAIKA  
RIGAEGPVS LVSTGCTSGLDVAGRAA-DLIAEGAADVMLAGATEAPISPIITVACFDAIKA  
-AGAEGPVTVSTGCTSGLDVAGYGT-ELIRDGRADVVCATDAPISPIITVACFDAIKA  
-AGAEGPVNIVSAGCTSGIDSIGYAC-ELIREGTVDMVLAGGVADAPITVACFDAIRV  
-AGAEGPVNIVSAGCTSGIDSIGYAC-ELIREGTVDMVAGGVADAPITVACFDAIRA  
-FGVRGPVQTVSTGCTSGLDVAGYAY-HAVAEGRVDCLAGAADSPISPIITMACFDAIKA



KCLFDAU  
KCLFPEU  
KCLFACT  
KCLFHIR  
KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE

RLSGSDDPDTAGYLPFDRRAAGHVPGE-GAILAVEDAERVAERG-GKVYGSIAGT-ASFD  
RLSGSDNPTAGYLPFDRRAAGHVPGE-GAILTVEDAERAAERG-AKVYGSIAGYASFD  
RISTATDPDRAYLPFDERAAGYVPGEG-GAILVLEDSAAAEARGHRDAYGELAGCASTFD  
RVSRATDPGRAYLPFDVAANGYVPGEG-GAILLLEDAESAKARG-ATGYGEIAGYATFTD  
LVSTVADPERAYLPFDVDASGYVPGEG-GAVLIVEDADSARARG--AERYVRSPLRRD  
GLSTSDDPDRAYLPFDAAAGHVPGE-GALLVLESDSARARGVTRWYGRIDGYAATFD  
FLSEATDPHDAYLPFDARAAGYVPGEG-GAMVAERADSARERDAATVYGRIGIAGHASTFD  
-MSDSDEPNRAYLPFDRDGRGYVPGGGRGVPPLEAEAAAPARG-AEYVGE-AGPLARL-  
RLSTSEEPARGYLPFDREAQGHVPGE-GAILVMEAAEAARERG-ARIYGEIAGYGSTFD  
ELSRATEPDRAYRPFTEACGFAPAEG-GAVLVVEEEAAARERG-ADVRA TVAGHAATFT

Fig 2B

09/720841

KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

TTPRNDPAHASRPFDRNGFVLAEG-AAMFVLEEEYAAQRRG-AHIYAEVGGYATRSQ  
TTPRNDDEHASRPFDRNGFVLAEG-AALFVLEEELEHARARG-AHVYAEISGCATRLN  
TTARNDDPEHASRPFDRNGFVLAEG-AAMFVLEEDYDSALARG-ARIHAEISGYATRCN  
TTPRHDAPATASRPFDRNGFVLAEG-AAFFVLEELHSARRRG-AHIYAEIAGYATRSN  
TINRYDDPAHASRPFDRNGFVLAEG-AAVFLVLEELLESARARG-AHIYAEIAGYATRSN  
TTPRNDTPAEASRPFDRNGFVLAEG-AAVFLVEEFHARRRG-ALVYAEIAGFATRCN  
TSANNDPAHASRPFDRNGFVLAEG-SAVFVLEELSAARRRG-AHAYAEVRGFATRSN  
TSDHNDTPETLA-PFSRNRNGFVLAEG-GAIVVLEEEAAVRRG-ARIYAEIGGYASRGN  
TSDHNDTPETASRPFDRNGFVLAEG-GAIVVLEEEAAVRRG-ARIYAEIGGYASRGN  
TSPNNDPAHASRPFDRNGFVLAEG-AAVLVLEEDLEHARARG-ADVCEVSGYATFCN

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KCLFDAU  
KCLFPEU  
KCLFACT  
KCLFHIR  
KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE  
KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

-PPPGSGRP---SALARAVETALADAGLDRSDIAVVFADGAA-VGELDVAEAEALASVFG  
-PPPGSGRP---SALARAVETALADAGLDGSDIAVVFADGAA-VPELDAAEAEALASVFG  
-PAPGSGRP---AGLERAI RLALNDAGTGPEVDVVFADGAG-VPELDAAEARAIGRVFG  
-PAPGSRP---PALRRAI ELALADAELRPEQVDVVFADAG-VAELDAIEAAAI RELFG  
-PAPGSGRP---PALGRAAEALAEAGLTPADISVVFADGAG-VPELDRAEADTLARLFG  
-PPPGSGRP---PNLLRAAQALDDAEVGP EAVDVVFADAG-TPEDAEAEADAVRRLFG  
-ARPGTGRP---TGPARAI RLALAEARVAPEDVDVVFADAG-VPALDRAEAEALAEVFG  
-PAPHSRG---STRAHAIR TALDDAGTAPGDIRRVFADGGGRYPN-DRAEAEAI SEVFG  
-PRPGSGRE---PGLRKAI ELALADAGAAPGDI DVVFADAAA-VPELDRVEAEALNAVFG  
GAGRWAESR---EGLARAI QGALAEAGCRPEEVDVVFADALG-VPEADRAEALALADALG  
-AYHMTGLKKGREMAESIRALDEARLDRTAVDYVNAHGSG-TKQNDRHETA AFKRS LG  
-AYHMTGLKTDGREMAEAI RVALDLARIDPTDIDYINAHGSG-TKQNDRHETA AFKRS LG  
-AYHMTGLKADGREMAETIRVALDESRTDATDIDYINAHGSG-TQNDRHETA AYKRALG  
-AYHMTGLR-DGAEMAEAI RLALDEARLNPEQVDYINAHGSG-TKQNDRHETA AFKKALG  
-AYHMTGLRPGDGAEMAEAI RVALDEARMNPTEIDYINAHGSG-TKQNDRHETA AFKKSLG  
-AFHMTGLRPGDGREMAEAI GVALAQAGKAPADVDYVNAHGSG-TQNDRHETA AFKRS LG  
-AFHMTGLKPGDGREMAEAI TAALDQARRTGDDLHYINAHGSG-TQNDRHETA AFKRS LG  
-AYHMTGLRADGAEMAAAI TAALDEARRDP SDVDYVNAHGTA-TQNDRHETS AFKRS LG  
-AYHMTGLRADGAEMAAAI TAALDEARRDP SDVDYVNAHGTA-TQNDRHETS AFKRS LG  
-AYHMTGLTKEGLEMARAI DTALDMAELDGS AIDYVNAHGSG-TQNDRHETA AVKRS LG

. : \* : : \* . . \* \* : \*

Fig 2c

09/720841

KCLFDAU  
KCLFPEU  
KCLFACT  
KCLFHIR  
KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE  
KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

P--HRVPVTVPKLTGRLYSAGPLDVATGLLALRDEVVPATGHVH-PDPDLPLDVVTGR  
P--RRVPVTVPKLTGRLYSAGPLDVATALLALRDEVVPATAHVD-PDPDLPLDVVTGR  
R--EGVPVTVPKLTGRLYSAGGGLDVVTALMSLREGVIAPTAGVTSVPREYGIDLVLGE  
P--SGVPVTVPKLTGRLYSAGGGLDLVAALLAIRDGVIPTVHTAEPVPEHQDLVLTGD  
P--RGVPVTVPKALTGRLCAGGPPADLAAALLALRDQVIPTGRHRAVPDAYALDLVTGR  
P--YGVPVTVPKLTGRLSAGGAALDVATALLALREGVVPPTVNVSRPRPEYELDLVLA-  
P--GAVPVTVPKLTGRLYAGGAALDVATALLSIRDCVVPPTVGTGAPAPGLGIDLVLHQ  
P--GRVPVTVCPRTMTGRLHSGAAPLDVACALLAMRAGVIPTVHID-PCPEYDLDLVLYQ  
T--GAVPVTVPKLTGRLYSGAAPLDLAAAFAMDEGVIPTVNVE-PDAAYGLDLVVGG  
PHAAVVPVTVPKLTGRLYCAAPVLDVATAVLAMEHGLIPTPHVL--DVCHDLDLVTGR  
EHAYAVPVSSIKSMGGHSLGAIGSIEIAASVLAIEHNVVPPTANLHTPDPECDLDYVPLT  
EHAYRTPVSSIKSMVGHSLGAIGSIEVAACALAIHGVVPPTANLHEPDPECDLDYVPLT  
EHARRTPVSSIKSMVGHSLGAIGSIEIAACVLAIEHGVVPPTANLRTSDPECDLDYVPLE  
EHAYRTPVSSIKSMVGHSLGAIGSIEIAASALAMEYDVVPPTANLHTPDPECDLDYVPLT  
DHAYRTPVSSIKSMVGHSLGAIGSIEIAASALAMEHNVVPPTGNLHTPDPECDLDYVR-S  
DHAYRVPVSSIKSMIGHSLGAIGSLEIAASVLAITHDVVPPTANLHEPDPECDLDYVPLR  
QRAYDVVPVSSIKSMIGHSLGAIGSLEIAACALAIHGVIPPTANYEEDPECDLDYVPLR  
DHAYRVPVSSIKSMIGHSLGAAGSLEVAATALAVEYGAIPPTANLHDPPELDLDYVPLT  
EHAYRVPVSSIKSMIGHSLGAVGSLEVAATALAVEYGVIPPTANLHDPPELDLDYVPLT  
EHAYATPMSSIKSMVGHSLGAIGSIEIAACVLAIAHQVVPPTANYTTPDPECDLDYVPRE  
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KCLFDAU  
KCLFPEU  
KCLFACT  
KCLFHIR  
KCLFGRA  
KCLFNOG  
KCLFTCM  
KCLFCIN  
KCLFVNZ  
KCLFWHIE  
KSGRA  
KSHIR  
KSACT  
KSCIN  
KSVNZ  
KSNOG  
KSTCM  
KSDAU  
KSPEU  
KSWHI

PRAMADARAALVVARGHGGFNSALVVRGAA-----  
PRSLADARAALLVARGYGGFNSALVVRGAA-----  
PRSTAPRTA-LVLARGRWGFNSAAVLRRAFPTP----  
PRHQQLGTA-LVLARGKWGFNSAVVVRGVGTG-----  
PREAALSAA-LVLARGRHGFNSAVVVTLRGSDHRRPT  
PRRTPLARA-LVLARGRGGFNSAAMVVGAPRAETR---  
PRELRVDTA-LVVARGMGGFNSALVVRRHG-----  
VRPAALRTA-LGGARGHGGFNSALVVRAGQ-----  
PRTAEVNTA-LVLRARGHGGFNSAMVVRSAN-----  
ARPAEPRTA-LVLARGLMGSNSALVLRGAVPPEGR-  
AREQRVDTV-LTVGSGFGGFQSAMVLRHPEEAA----  
AREQRVDTV-LSVSGSGFGGFQSAMVLRRLGGANS---  
ARERKLRVS-LTVGSGFGGFQSAMVLRDAETAGAAA-  
ARDQRVDSV-LTVGSGFGGFQSAMVLTSAQ---RSTV  
CREQLTDSV-LTVGSGFGGFQSAMVLARPE---RKIA  
ARACPVDTV-LTVGSGFGGFQSAMVLCGPGSRGRSAA  
AREQRVDTV-LSVSGSGFGGFQSAVVLARPKETRS---  
AREKRVRHA-LTVGSGFGGFQSAMLLSRPER-----  
AREKRVRHA-LTVGSGFGGFQSAMLLSRLEP-----  
ARERTLRHV-LSVSGSGFGGFQSAVVLSGSEGGLR---  
\* . \* . \* \* : : \* : :

mole:-/ks2%

Fig 2D

[illegible]

The diagram illustrates the domain architecture and organization of the *srm* gene family. The top part shows the domain architecture of *srmGl*, *srmGII*, *srmGIII*, *srmGIV*, and *srmGV*. Domains are represented by circles with labels: KSa, AT, ACP, KS, KR, DH, KR, ER, and TE. The bottom part shows the organization of the *srm* gene cluster on a chromosome, with modules 1 through 7 corresponding to the domains above. *srmGI* contains modules 1 and 2, *srmGII* contains module 3, *srmGIII* contains modules 4 and 5, *srmGIV* contains module 6, and *srmGV* contains module 7. A scale bar indicates 10 kb.

Fig 3

m: malonyl transferase  
mm: methylmalonyl transferase  
em: ethylmalonyl transferase  
C2: unknown C2 unit transferase

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Fig. 4A

	1					50
niddamycin	-----	-----	MAGHGDATAQ	KAQDAEKSED	GSDAIAVIGM	
platenolide	-----	-----	-----MS	GELAISRSDD	RSDAVAVVGM	
monensin	-----	-----	-----MAAS	ASASPSGPSPA	GPDPIAVVGM	
oleandomycin	-----	-----	-----	---MHVPGEE	NGHSIAIVGI	
tylosin	MSSALRRRAVQ	SNCGYGDLMT	SNTAAQNTGD	QEDVDGPDST	HGGEIAVVGM	
	51					100
niddam...	SCRFPGAPGT	AEFWQLLSSG	ADAVVTAADG	RRR.....	.....GTIDA	
platenol.	ACRFPGAPGI	AEFWKLLTDG	RDAIGRDADG	RRR.....	.....GMIEA	
monensin	ACRLPGAPDP	DAFWRLLESG	RSVSTAPPE	RRRADSGLHG	P...GGYLDR	
oleandom	ACRLPGSATP	QEFWRLLADS	ADALDEPPAG	RFPTGSLSSP	PAPRGGFLDS	
tylosin	SCRLPGAAGV	EEFWELLRS	RGMPTRQDDG	TWRAA.....	.....LED	
	101					150
niddam...	PADFDAAFFG	MSPREAAATD	PQORLVLELG	WEALEDAGIV	PESLRGEAAS	
platenol.	PGDFDAAFFG	MSPREAAETD	PQORLMLELG	WEALEDAGIV	PGSLRGEAVG	
monensin	IDGFDADFFH	ISPRAVAMD	PQORLLELS	WEALEDAGIR	PPTLARSRTG	
oleandom	IDTFDADFFN	ISPRAEAGVLD	PQORLLELG	WEALEDAGIV	PRHLRGTRTS	
tylosin	HAGFDAGFFG	MNARQAAATD	PQHRLMLELG	WEALEDAGIV	PGDLTGTDG	
	151					200
niddam...	VFVGAMNDY	ATLLH.RAGA	PTDITYTATGL	QHSMIANRLS	YFLGLRGPSL	
platenol.	VFVGAMHDDY	ATLLH.RAGA	PVGPHATATGL	QRAMLNRLS	YVLGTRGPSL	
monensin	VFVGAFWDDY	TDVLNLRAPG	AVTRHTMTGV	HRSILANRLS	YAYHLAGPSL	
oleandom	VFMGAMWDDY	AHLAHARGE	ALTRHSLTGT	HRGMIANRLS	YALGLQGPSL	
tylosin	VFAGVASDDY	A.VLTRRSV	SAGGYTATGL	HRALANRLS	HFLGLRGPSL	
	201					250
niddam...	VVDTGQSSSL	VAVALAVESL	RGGTSGIALA	GGVNLVLAEE	GS.AAMERVG	
platenol.	AVDTAQSSSL	VAVALAVESL	RAGTSRVAVA	GGVNLVLADE	GT.AAMERLG	
monensin	TVDTAQSSSL	VAVHLACESI	RSGSDIAFA	GGVNLICSPR	TTELAARFG	
oleandom	TVDTGQSSSL	AAVHMACESL	ARGESDLALV	GGVNLVLDPA	GT.TGVERFG	
tylosin	VVDSAQSASL	VAVQLACESL	RRGETSLAVA	GGVNLILTEE	ST.TVMERMG	
	251					300
niddam...	ALSPDGRCHT	FDARANGYVR	GEGGAIIVLK	PLADALADGD	RVYCVVRGVA	
platenol.	ALSPDGRCHT	FDARANGYVR	GEGGAIVLK	PLADALADGD	PVYCVVRGVA	
monensin	GLSAAGRCHT	FDARADGFVR	GEGGGLVVLK	PLAAARRDGD	TVYCVIRGSA	
oleandom	ALSPDGRCHT	FDSRANGYAR	GEGGVVVVLK	PTHRALADGD	TVYCEILGSA	
tylosin	ALSPDGRCHT	FDARANGYVR	GEGGGAIVLK	PLDAALADGD	RVYCVIKGGA	
	301					350
niddam...	TGNDGGGPGL	TVPDRAGQEA	VLRAACDQAG	VRPADVRFVE	LHGTGTPAGD	
platenol.	VGNDGGGPGL	TAPDREGQEA	VLRAACAQAR	VDPAEVRFVE	LHGTGTPVGD	
monensin	VNSDGTDDGI	TLPSGQAQD	VVRLACRRAR	ITPDQVQYVE	LHGTGTPVGD	
oleandom	LNNDGATEGL	TVPSARAQAD	VLRQAWERAR	VAPTDVQYVE	LHGTGTPAGD	
tylosin	VNNDGGGASL	TTPDREAQEA	VLRQAYRRAG	VSTGAVRYVE	LHGTGTRAGD	

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	351		400
niddam...	PVEAEALGAV YGTGRP..AN EPLLVGSVKT NIGHLEGAAG	IAGFVKAALC	
platenol.	PVEAHALGAV HGSGRP..AD DPLLVGSVKT NIGHLEGAAG	IAGLVKAALC	
monensin	PIEAAALGAA LGQDAA..RA VPLAVGSAKT NVGHLEAAAG	IVGLLKLTALS	
oleandom	PVEAEGLGTA LGTARP..AE APLLVGSVKT NIGHLEGAAG	IAGLLKTVLS	
tylosin	PVEAAALGAV LGAGADSGRS TPLAVGSVKT NVGHLEGAAG	IVGLIKATLC	
	401		450
niddam...	LHERALPASL NFETPNPAIP LERLRLKVQT AHAALQPGTG	GGPLLAVGSA	
platenol.	LRERTLPGSL NFATPSAIP LDQLRLKVQT AAAELPLAPG	GAPLLAGVSS	
monensin	IHHRR LAPSL NFFTNPAP	LADLGLTVQQ DLADWP..RP	EQPLIAGVSS
oleandom	IKNRHLPASL NFTSPNPRID LDALRLRVHT AYGPWP..SP	DRPLVAGVSS	
tylosin	VRKGELVPSL NFSTPNPDIP LDDLRLRVQT ERQEW.NEED	DRPRVAGVSS	
	451		500
niddam...	FGMGGTNCHV VLEETPGG..	.....RQPAE.T	
platenol.	FGIGGTNCHV VLEHLPSR..	.....PTPAV.S	
monensin	FGMGGTNCHV VVA....AAP DSVAVPEPVG VPERVEVPEP	VVVSEPVVVP	
oleandom	FGMGGTNCHV VLSELRNAGG DGAGKGPYTG TEDRLGATEA	EKRDPDPATGN	
tylosin	FGMGGTNVHL VIAEAPAAAG SSGAGGSGAG SGAGISAVSG	VV.....	
	501		550
niddam...	GQADACLFSA SPMLLLSARS EQALRAQAAR LREHL..EDS	GADPLDIAYS	
platenol.	VAAS...LPD VPPLLLSARS EGALRAQAVR LGETV..ERV	GADPRDVAYS	
monensin	TPWP.....VSAS ASALRAQAGR LRTHLAAHRP	TPDAARVGHA	
oleandom	GPDPAQDTHR YPALILSARS DAALRAQAER LRHHL.EHSP	GQRLRDTAYS	
tylosin	.....PVVVSGRS RVVVREAAGR LAE..VVEAG	GVGLADVAVT	
	551		600
niddam...	LATTRTRFEH RAAVPCGDPD RLSSALAALA AGQTPRGVRI	GS..TDADGR	
platenol.	LASTRTLFEH RAVVPCGGRG ELVAALGGFA AGRVSGGVRS	GR..A.VPGG	
monensin	LATTRAPLAH RAVLLGGDTA ELLGSLDALA EGAETASIVR	GEAYT..EGR	
oleandom	LATRRQVFER HAVVTGHDRE DLLNGLRDLE NGLPAPQVLL	GRTPTPEPGG	
tylosin	MAD.RSRFGY RAVVLARGEA ELAGRLRALA GGDPDAGVVT	G...AVLDGG	
	601		650
niddam...	LALLFTGQGA QHPGMGQELY TTDPHFAAAL DEVCEELQRC	GTQNLREVMF	
platenol.	VGVLFTGQGA QWVGMRGLY AGGGVFAEVL DEVLSMVGEV	DGRSLRDVMF	
monensin	TAFLFSGQGA QRLGMGRELY AVFPVFADAL DEAFALDVH	LDRPLREIVL	
oleandom	LAFLFSGQGS QQPGMGKRLH QVFPGFRDAL DEVCAELDTH	LGRL.....	
tylosin	VVGAAPGGA GAAGGAGAAG GAGGGGVVLV FPGQGTQWVG	MGAGLLGSSE	
	651		700
niddam...	TPDQPD....	.....LLDRTEYTQP	ALFALQTALY
platenol.	GDVDVDAGAG ADAGAGAGAG VGSGSGSVGG LLGRTEFAQP	ALFALEVALF	
monensin	GETDSGGNVS GENVIGEGA. ....DHQA LLDQTAYTQP	ALFAIETSLY	
oleandom	.GPEAGPPLR DVMFAERGT. ....AHSA LLSETHYTQA	ALFALETALF	
tylosin	VFAASMRECA RALSVHVGWD LLEVVSAGGAG .LERVDVVQP	VTWAVMVSLA	
	701		750
niddam...	RTLTARGETQA HVLVGHVSVE ITAAHIAGVL DLPDAARLIT	ARAHVMGQLP	
platenol.	RALEARGVEV SVVLGHVSVE VAAATVAGVL SLGDAVRLVV	ARGGLMGGLP	
monensin	RLAASFGLKP DYVLGHVSVE IAAAHVAGVL SLPDASALVA	TRGRLMQAVR	
oleandom	RLLVQWGLKP DHLAGHSVE IAAHAAGIL DLSDAAEVLA	TRGALMRSLP	
tylosin	RYWQAMGVDV AAVVGHVSQGE IAAATVAGAL SLEDAAVVA	LRAGLIGRYL	

Fig 4B



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	751		800
niddam...	HG.GAMLSVQ	AAEHDLQDLA	HTHG..VEIA
platenol.	VG.GGMWSVG	ASESVVRGVV	EGLGEWVSVA
monensin	AP.GAMAAWQ	ATADEAAEQ	AGHERHVTVA
oleandom	GG.GVMLSVQ	APESVAPLL	LGREAHVGLA
tylosin	AGRGAMAAVP	LPAGEVEAGL	.AKWPGVEVA
			AVNGPTHCVL
			SGPRTALEET
			SGDVGVLESV
			SGDRATVDEL
			SGERGHVAAI
			SGDRRAVAGY
	801		850
niddam...	AQHLREQNVR	HTWLKVSHAF	HSALMDPMLG
platenol.	VASLMGDGVE	YRRLDVSHGF	HSVLMPEVLG
monensin	TAAWRGRGRK	AHHLKVSHAF	HSPHMDPILD
oleandom	EQILRDRGRK	SRYLRVSHAF	HSPLMPEVLE
tylosin	VAVCQAEVQ	ARLIPVDYAS	HSRHVEDLKG
			ELERVLSGI.
			.RPRSPRPV
	851		900
niddam...	ISNLTGQIA.	.....DPNHL	CTPDYWIDHA
platenol.	VSGVSGGVV.	.....GSGEL	GDPGYWVRHA
monensin	VSNVTGELVT	ATATGSGAGQ	ADPEYWARHA
oleandom	VSNLTG....	..APVDDRTM	ATPAYWVRHV
tylosin	CSTVAGEQPG	EPVF.....	.DAGYWFRNL
			RNRVEFSAVV
			GGLLEEGRH
	901		950
niddam...	YLEIGPHPTL	TTLHHTL..	.DNP.....
platenol.	LVEVGPHGVL	TGMAGECLGA	GDDV.....
monensin	FVELGPDAPL	SAMARDCFPA	P.....
oleandom	FLEVGPDGVL	TAMARACVTA	APEPGHRGEQ
tylosin	FIEVSAHPVL	V.....	.....HAIEQ
			TAEAADRSVH
			ATGTLRRQDD
	951		
niddam...	EPETLTQAIA	AVGVRTDGID	WAVLCGASRP
platenol.	EREVFEEALA	TVFTRDAGLD	ATALHTGSTG
monensin	EVATFLRSLA	QAYVRGADVD	FTRAYGATAT
oleandom	EARSLTEAVA	RLHLHGVPMD	WTSVLGGDVS
tylosin	SPHRLLTSTA	EAWAHGATLT	WDPAL..PPG
			HLTTLPTYPF

niddam: niddamycin; platenol: platenolide I (spiramycin); oleandom:  
oleandomycin.

FIG. 4C

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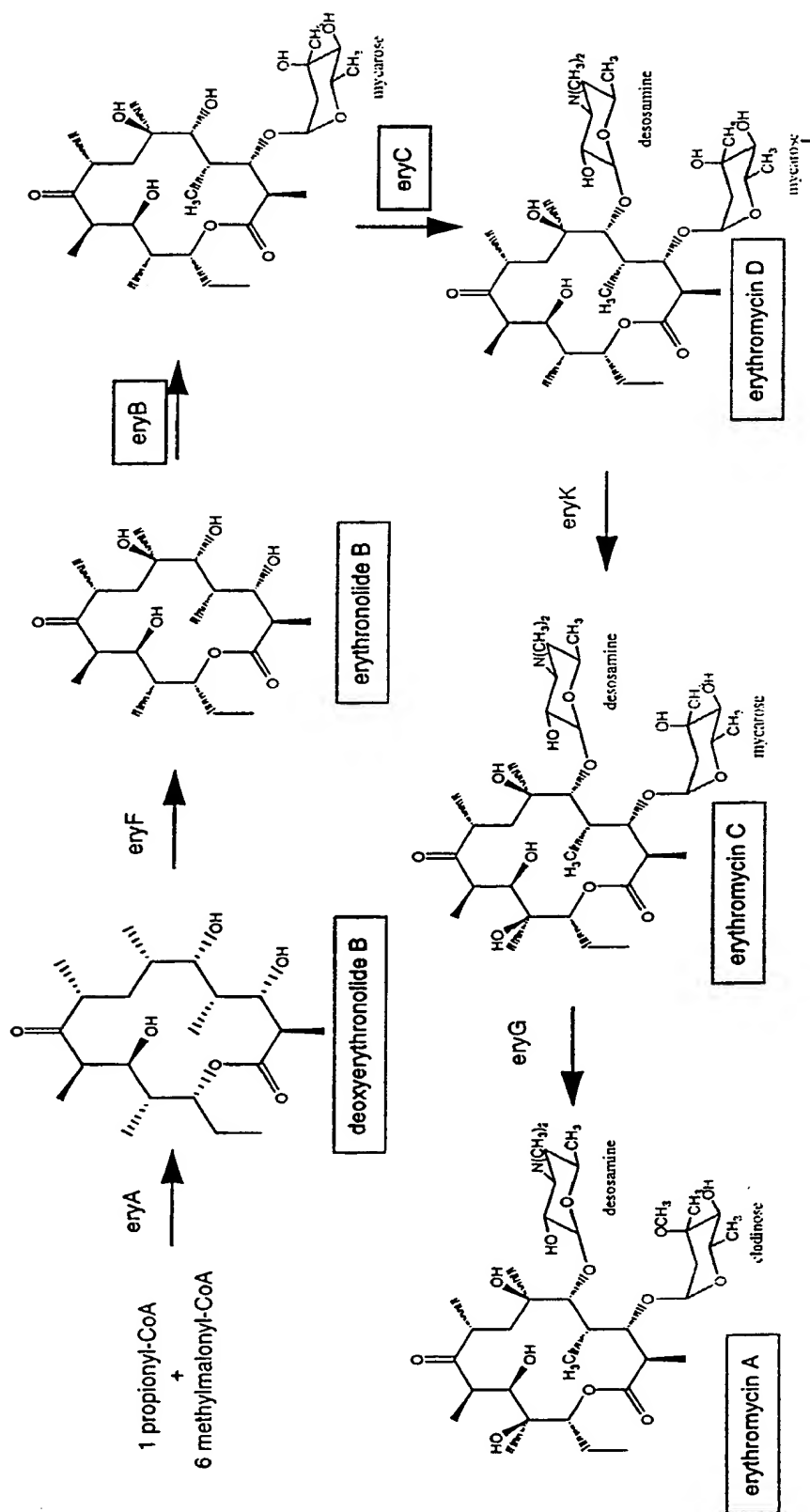


Fig. 5



Fig 6

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Figure 7

forward (Plf):

5'-CTA GGC CGG GCC GGA CTG GTA GAT CTG CCT ACG TAT CCT TTC CAG GGC AAG CGG TTC TGG CTG CAG CCG GAC CGC ACT AGT CCT CGT GAC GAG

GGA GAT GCA TCG AGC CTG AGG GAC CGG TT-3'

backward (Plb):

5'-AAC CGG TCC CTC AGG CTC GAT GCA TCT CCC TCG TCA CGA GGA CTA GTG CGG TCC GGC TGC AGC CAG AAC CGC TTG CCC TGG AAA GGA TAC GTA

GGC AGA TCT ACC AGT CCG GCC CGG C-3'

oligos annealed:

CTAGCCCGGCGGACTGCTAGATCTGCCTACGTATCCTTTCCAGGGCAAGCGGTTCTGGCTGCAGCCGACCGCACTAGTCTCTGTGACGAGGAGATGCATCGAGCCCTGAGGGACCGGTT  
CGGCCCGGCGGCGGACTGCTAGATCTGCCTACGTATCCTTTCCAGGGCAAGCGGTTCTGGCTGCAGCCGACCGCACTAGTCTCTGTGACGAGGAGATGCATCGAGCCCTGAGGGACCGGTT

AvrII	BglII	SnaBI	PstI	SpeI	NsiI	Bsu36I	HpaI
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